

11-88L.ST25.txt  
SEQUENCE LISTING

<110> Seed, Brian  
Aruffo, Alejandro  
Camerini, David

<120> CD27 Coding Sequence

<130> 11-88L

<140> US 09/836,544

<141> 2001-04-17

<150> US 07/983,647

<151> 1992-12-01

<150> US 07/553,759

<151> 1990-07-13

<150> US 07/498,809

<151> 1990-03-23

<150> US 07/379,076

<151> 1989-07-13

<150> US 07/160,416

<151> 1988-02-25

<160> 41

<170> PatentIn version 3.3

<210> 1

<211> 2932

<212> DNA

<213> artificial

<220>

<223> Nucleotide sequence of piH3 vector

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gtcttaccgg gttggactca agacgatagt taccggataa ggcgagcgg tcgggctgaa	300
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## 11-88L.ST25.txt

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## 11-88L.ST25.txt

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<220>
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<222> (7)..(1059)

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Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
15 20 25 30

ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct 144
Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
35 40 45

agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act 192
Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr
50 55 60

tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc 240
Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe
65 70 75

aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att 288
Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile
80 85 90

aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat 336
Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr
95 100 105 110

gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att 384
Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile
115 120 125

caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca 432
Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr
130 135 140

acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg 480
Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu

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11-88L.ST25.txt

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aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys 195 200 205			624
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aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His 240 245 250			768
aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala 255 260 265 270			816
tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro 275 280 285			864
ggc cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His 290 295 300			912
cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcg ggc aca Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr 305 310 315			960
caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln 320 325 330			1008
cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser 335 340 345 350			1056
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11-88L.ST25.txt

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<212> PRT  
<213> Homo sapiens

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Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe  
35 40 45

Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp  
50 55 60

Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu  
65 70 75 80

Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His  
85 90 95

Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr  
100 105 110

Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu  
115 120 125

Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu  
130 135 140

Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln  
145 150 155 160

Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp  
165 170 175

Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val  
180 185 190

Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu  
195 200 205

11-88L.ST25.txt

Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met  
 210 215 220

Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln  
 225 230 235 240

Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val  
 245 250 255

Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr  
 260 265 270

Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His  
 275 280 285

Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val  
 290 295 300

Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val  
 305 310 315 320

His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys  
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Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn  
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 <222> (13)..(723)

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 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe  
 15 20 25

tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta 147  
 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val  
 30 35 40 45

cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195  
 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp

## 11-88L.ST25.txt

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aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac	291														
Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr															
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aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat	339														
Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn															
	95	100	105												
att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca	387														
Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro															
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tct ccc aca cta act tgt gca ttg act aat gga agc att gaa gtc caa	435														
Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln															
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Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr															
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Ser Trp Asp Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile															
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Tyr Phe Lys Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu															
	175	180	185												
agc aat cca tta ttt aat aca aca tca tca atc att ttg aca acc tgt	627														
Ser Asn Pro Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys															
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Ile Pro Ser Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile															
	210	215	220												
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Pro Leu Ala Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Val Leu															
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<210> 5  
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 <213> Homo sapiens

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11-88L.ST25.txt

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln  
20 25 30

Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn  
35 40 45

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala  
50 55 60

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg  
65 70 75 80

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr  
85 90 95

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp  
100 105 110

Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr  
115 120 125

Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile  
130 135 140

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp  
145 150 155 160

Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys  
165 170 175

Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro  
180 185 190

Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser  
195 200 205

Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala  
210 215 220

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<223> Nucleotide sequence of the pIH3M vector.

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## 11-88L.ST25.txt

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## 11-88L.ST25.txt

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1 5

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tcc ctt cac aaa gga ctg gat agt gct gtg gaa gtc tgt gtt gta tat 306  
Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu Val Cys Val Val Tyr  
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11-88L.ST25.txt

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Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg	185	190	195	
cgc ccc ggg ccc acc cgc aag cat tac cag ccc tat gcc cca cca cgc				738
Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg	200	205	210	
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Asp Phe Ala Ala Tyr Arg Ser	215	220		
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Asp	Asn	Ala	Val	Asn	Leu	Ser	Cys	Lys	Tyr	Ser	Tyr	Asn	Leu	Phe	Ser
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11-88L.ST25.txt

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Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser  
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Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met  
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## 11-88L.ST25.txt

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## 11-88L.ST25.txt

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Met Thr Thr Pro Arg Asn Ser  
1 5

gta aat ggg act ttc ccg gca gag cca atg aaa ggc cct att gct atg 162  
Val Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met  
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Gln Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Ser Ser Leu Val Gly  
25 30 35

ccc acg caa agc ttc ttc atg agg gaa tct aag act ttg ggg gct gtc 258  
Pro Thr Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val  
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cag att atg aat ggg ctc ttc cac att gcc ctg ggg ggt ctt ctg atg 306  
Gln Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met  
60 65 70

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75 80 85

ctc tgg gga ggc att atg tat att att tcc gga tca ctc ctg gca gca 402  
Leu Trp Gly Gly Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu Ala Ala  
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acg gag aaa aac tcc agg aag tgt ttg gtc aaa gga aaa atg ata atg 450  
Thr Glu Lys Asn Ser Arg Lys Cys Leu Val Lys Gly Lys Met Ile Met  
105 110 115

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140 145 150

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Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys  
155 160 165

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 Page 17

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25

30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu  
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Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile  
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Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu  
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Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly  
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Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile  
          195                         200                         205

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## 11-88L.ST25.txt

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11-88L.ST25.txt

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Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu Thr Pro Leu 50 55 60

11-88L.ST25.txt

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Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu  
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Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg  
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210 215 220

Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp  
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Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp  
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Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala  
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Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu  
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Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr  
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355 360 365

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Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu Lys Cys Leu  
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## 11-88L.ST25.txt

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1921

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catgcagaga	aaaacagtac	ctaataaaca	gtcagtgctg	ttctttgtgc	cagccaggac		180
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cctgcccagt	cggcttcttc	tccaatgtgt	catctgcttt	cgaaaaatgt	cacccttgga		540
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tgtggccacg tgggcaaaca ggcagttggc cagagagcct ggtgctgctg ctgcaggggt	960
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gaaccagagc ttgtagaac cactttaatc atatccagga gtttgcaaga aacaggtgct	180
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Met Gly Cys Asp Arg Asn Cys Gly	
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Leu Ile Ala Gly Ala Val Ile Gly Ala Val Leu Ala Val Phe Gly Gly	
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Ile Leu Met Pro Val Gly Asp Leu Leu Ile Gln Lys Thr Ile Lys Lys	
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Gln Val Val Leu Glu Glu Gly Thr Ile Ala Phe Lys Asn Trp Val Lys	
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Thr Gly Thr Glu Val Tyr Arg Gln Phe Trp Ile Phe Asp Val Gln Asn	
60 65 70	
cca cag gaa gtg atg atg aac agc agc aac att caa gtt aag caa aga	474
Pro Gln Glu Val Met Met Asn Ser Ser Asn Ile Gln Val Lys Gln Arg	
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ggc cct tat acg tac aga gtt cgt ttt cta gcc aag gaa aat gta acc	522
Gly Pro Tyr Thr Tyr Arg Val Arg Phe Leu Ala Lys Glu Asn Val Thr	
90 95 100	
cag gac gct gag gac aac aca gtc tct ttc ctg cag ccc aat ggt gcc	570
Gln Asp Ala Glu Asp Asn Thr Val Ser Phe Leu Gln Pro Asn Gly Ala	

## 11-88L.ST25.txt

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gtt Val	ctc Leu	aat Asn	ctg Leu 140	gct Ala	gtg Val	gca Ala	gct Ala	gca Ala 145	tcc Ser	cat His	atc Ile	tat Tyr	caa Gln 150	aat Asn	caa Gln	666	
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cca Pro 185	ttt Phe	ttg Leu	agt Ser	ttg Leu	gtt Val 190	ccg Pro	tac Tyr	cct Pro	gtt Val	act Thr 195	acc Thr	aca Thr	gtt Val	ggt Gly	ctg Leu 200	810	
ttt Phe	tat Tyr	cct Pro	tac Tyr	aac Asn 205	aat Asn	act Thr	gca Ala	gat Asp	gga Gly 210	gtt Val	tat Tyr	aaa Lys	gtt Val	ttc Phe 215	aat Asn	858	
gga Gly	aaa Lys	gat Asp	aac Asn 220	ata Ile	agt Ser	aaa Lys	gtt Val	gcc Ala 225	ata Ile	atc Ile	gac Asp	aca Thr	tat Tyr 230	aaa Lys	ggt Gly	906	
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aca Thr 250	gat Asp	gca Ala	gcc Ala	tca Ser	ttt Phe	cca Pro 255	cct Pro	ttt Phe	gtt Val	gag Glu	aaa Lys 260	agc Ser	cag Gln	gta Val	ttg Leu	1002	
cag Gln 265	ttc Phe	ttt Phe	tct Ser	tct Ser	gat Asp 270	att Ile	tgc Cys	agg Arg	tca Ser	atc Ile 275	tat Tyr	gct Ala	gta Val	ttt Phe	gaa Glu 280	1050	
tcc Ser	gac Asp	gtt Val	aat Asn	ctg Leu 285	aaa Lys	gga Gly	atc Ile	cct Pro	gtg Val 290	tat Tyr	aga Arg	ttt Phe	gtt Val	ctt Leu 295	cca Pro	1098	
tcc Ser	aag Lys	gcc Ala	ttt Phe 300	gcc Ala	tct Ser	cca Pro	gtt Val	gaa Glu 305	aac Asn	cca Pro	gac Asp	aac Asn	tat Tyr 310	tgt Cys	ttc Phe	1146	
tgc Cys	aca Thr	gaa Glu 315	aaa Lys	att Ile	atc Ile	tca Ser	aaa Lys 320	aat Asn	tgt Cys	aca Thr	tca Ser	tat Tyr 325	ggt Gly	gtg Val	cta Leu	1194	
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cat His 345	ttt Phe	ctg Leu	tat Tyr	gca Ala	agt Ser 350	cct Pro	gat Asp	gtt Val	tca Ser	gaa Glu 355	cct Pro	att Ile	gat Asp	gga Gly	tta Leu 360	1290	
aac	cca	aat	gaa	gaa	gaa	cat	agg	aca	tac	ttg	gat	att	gaa	cct	ata	1338	

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Thr	Gly	Phe	Thr	Leu	Gln	Phe	Ala	Lys	Arg	Leu	Gln	Val	Asn	Leu	Leu	
			380					385					390			
gtc	aag	cca	tca	gaa	aaa	att	caa	gta	tta	aag	aat	ctg	aag	agg	aac	1434
Val	Lys	Pro	Ser	Glu	Lys	Ile	Gln	Val	Leu	Lys	Asn	Leu	Lys	Arg	Asn	
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Tyr	Ile	Val	Pro	Ile	Leu	Trp	Leu	Asn	Glu	Thr	Gly	Thr	Ile	Gly	Asp	
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Glu	Lys	Ala	Asn	Met	Phe	Arg	Ser	Gln	Val	Thr	Gly	Lys	Ile	Asn	Leu	
425				430						435					440	
ctt	ggc	ctg	ata	gaa	atg	atc	tta	ctc	agt	gtt	ggt	gtg	gtg	atg	ttt	1578
Leu	Gly	Leu	Ile	Glu	Met	Ile	Leu	Leu	Ser	Val	Gly	Val	Val	Met	Phe	
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			20					25					30			
Leu Ile Gln Lys Thr Ile Lys Lys Gln Val Val Leu Glu Glu Gly Thr																
		35					40					45				
Ile Ala Phe Lys Asn Trp Val Lys Thr Gly Thr Glu Val Tyr Arg Gln																
	50					55				60						
Phe Trp Ile Phe Asp Val Gln Asn Pro Gln Glu Val Met Met Asn Ser																
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Ser Asn Ile Gln Val Lys Gln Arg Gly Pro Tyr Thr Tyr Arg Val Arg  
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Phe Leu Ala Lys Glu Asn Val Thr Gln Asp Ala Glu Asp Asn Thr Val  
100 105 110

Ser Phe Leu Gln Pro Asn Gly Ala Ile Phe Glu Pro Ser Leu Ser Val  
115 120 125

Gly Thr Glu Ala Asp Asn Phe Thr Val Leu Asn Leu Ala Val Ala Ala  
130 135 140

Ala Ser His Ile Tyr Gln Asn Gln Phe Val Gln Met Ile Leu Asn Ser  
145 150 155 160

Leu Ile Asn Lys Ser Lys Ser Ser Met Phe Gln Val Arg Thr Leu Arg  
165 170 175

Glu Leu Leu Trp Gly Tyr Arg Asp Pro Phe Leu Ser Leu Val Pro Tyr  
180 185 190

Pro Val Thr Thr Thr Val Gly Leu Phe Tyr Pro Tyr Asn Asn Thr Ala  
195 200 205

Asp Gly Val Tyr Lys Val Phe Asn Gly Lys Asp Asn Ile Ser Lys Val  
210 215 220

Ala Ile Ile Asp Thr Tyr Lys Gly Lys Arg Asn Leu Ser Tyr Trp Glu  
225 230 235 240

Ser His Cys Asp Met Ile Asn Gly Thr Asp Ala Ala Ser Phe Pro Pro  
245 250 255

Phe Val Glu Lys Ser Gln Val Leu Gln Phe Phe Ser Ser Asp Ile Cys  
260 265 270

Arg Ser Ile Tyr Ala Val Phe Glu Ser Asp Val Asn Leu Lys Gly Ile  
275 280 285

Pro Val Tyr Arg Phe Val Leu Pro Ser Lys Ala Phe Ala Ser Pro Val  
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Glu Asn Pro Asp Asn Tyr Cys Phe Cys Thr Glu Lys Ile Ile Ser Lys  
305 310 315 320

Asn Cys Thr Ser Tyr Gly Val Leu Asp Ile Ser Lys Cys Lys Glu Gly



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ctg	ctc	ctt	tgg	gtt	cca	ggt	gat	ggg	caa	gtg	gac	acc	aca	aag	gca	102
Leu	Leu	Leu	Trp	Val	Pro	Val	Asp	Gly	Gln	Val	Asp	Thr	Thr	Lys	Ala	
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gtg	atc	tct	ttg	cag	cct	cca	tgg	gtc	agc	gtg	ttc	caa	gag	gaa	acc	150
Val	Ile	Ser	Leu	Gln	Pro	Pro	Trp	Val	Ser	Val	Phe	Gln	Glu	Glu	Thr	
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gta	acc	ttg	cac	tgt	gag	gtg	ctc	cat	ctg	cct	ggg	agc	agc	tct	aca	198

## 11-88L.ST25.txt

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aga Arg	atc Ile	acc Thr	tct Ser	gcc Ala 75	agt Ser	gtc Val	aat Asn	gac Asp	agt Ser 80	ggg Gly	gaa Glu	tac Tyr	agg Arg	tgc Cys 85	cag Gln	294
aga Arg	ggg Gly	ctc Leu	tca Ser 90	ggg Gly	cga Arg	agt Ser	gac Asp	ccc Pro 95	ata Ile	cag Gln	ctg Leu	gaa Glu	atc Ile 100	cac His	aga Arg	342
ggc Gly	tgg Trp	cta Leu 105	cta Leu	ctg Leu	cag Gln	gtc Val	tcc Ser 110	agc Ser	aga Arg	gtc Val	ttc Phe	acg Thr 115	gaa Glu	gga Gly	gaa Glu	390
cct Pro	ctg Leu 120	gcc Ala	ttg Leu	agg Arg	tgt Cys	cat His 125	gcg Ala	tgg Trp	aag Lys	gat Asp	aag Lys 130	ctg Leu	gtg Val	tac Tyr	aat Asn	438
gtg Val 135	ctt Leu	tac Tyr	tat Tyr	cga Arg	aat Asn 140	ggc Gly	aaa Lys	gcc Ala	ttt Phe	aag Lys 145	ttt Phe	ttc Phe	cac His	tgg Trp	aat Asn 150	486
tct Ser	aac Asn	ctc Leu	acc Thr	att Ile 155	ctg Leu	aaa Lys	acc Thr	aac Asn	ata Ile 160	agt Ser	cac His	aat Asn	ggc Gly	acc Thr 165	tac Tyr	534
cat His	tgc Cys	tca Ser	ggc Gly 170	atg Met	gga Gly	aag Lys	cat His	cgc Arg 175	tac Tyr	aca Thr	tca Ser	gca Ala	gga Gly 180	ata Ile	tct Ser	582
gtc Val	act Thr	gtg Val 185	aaa Lys	gag Glu	cta Leu	ttt Phe	cca Pro 190	gct Ala	cca Pro	gtg Val	ctg Leu	aat Asn 195	gca Ala	tct Ser	gtg Val	630
aca Thr	tcc Ser 200	cca Pro	ctc Leu	ctg Leu	gag Glu	ggg Gly 205	aat Asn	ctg Leu	gtc Val	acc Thr	ctg Leu 210	agc Ser	tgt Cys	gaa Glu	aca Thr	678
aag Lys 215	ttg Leu	ctc Leu	ttg Leu	cag Gln	agg Arg 220	cct Pro	ggg Gly	ttg Leu	cag Gln	ctt Leu 225	tac Tyr	ttc Phe	tcc Ser	ttc Phe	tac Tyr 230	726
atg Met	ggc Gly	agc Ser	aag Lys	acc Thr 235	ctg Leu	cga Arg	ggc Gly	agg Arg	aac Asn 240	aca Thr	tcc Ser	tct Ser	gaa Glu	tac Tyr 245	caa Gln	774
ata Ile	cta Leu	act Thr	gct Ala 250	aga Arg	aga Arg	gaa Glu	gac Asp	tct Ser 255	ggg Gly	tta Leu	tac Tyr	tgg Trp	tgc Cys 260	gag Glu	gct Ala	822
gcc Ala	aca Thr	gag Glu 265	gat Asp	gga Gly	aat Asn	gtc Val	ctt Leu 270	aag Lys	cgc Arg	agc Ser	cct Pro	gag Glu 275	ttg Leu	gag Glu	ctt Leu	870
caa Gln	gtg Val 280	ctt Leu	ggc Gly	ctc Leu	cag Gln	tta Leu 285	cca Pro	act Thr	cct Pro	gtc Val	tgg Trp 290	ttt Phe	cat His	gtc Val	ctt Leu	918

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Phe Tyr Leu Ala Val Gly Ile Met Phe Leu Val Asn Thr Val Leu Trp	
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gtg aca ata cgt aaa gaa ctg aaa aga aag aaa aag tgg gat tta gaa	1014
Val Thr Ile Arg Lys Glu Leu Lys Arg Lys Lys Lys Trp Asp Leu Glu	
315 320 325	
atc tct ttg gat tct ggt cat gag aag aag gta act tcc agc ctt caa	1062
Ile Ser Leu Asp Ser Gly His Glu Lys Lys Val Thr Ser Ser Leu Gln	
330 335 340	
gaa gac aga cat tta gaa gaa gag ctg aaa tgt cag gaa caa aaa gaa	1110
Glu Asp Arg His Leu Glu Glu Glu Leu Lys Cys Gln Glu Gln Lys Glu	
345 350 355	
gaa cag ctg cag gaa ggg gtg cac cgg aag gag ccc cag ggg gcc acg	1158
Glu Gln Leu Gln Glu Gly Val His Arg Lys Glu Pro Gln Gly Ala Thr	
360 365 370	
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Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln
50 55 60
Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser
65 70 75 80
Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile
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Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg
100 105 110
Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys

115                                      120                                      125  
 Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe  
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 Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile  
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 Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr  
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 Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro  
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 Val Leu Asn Ala Ser Val Thr Ser Pro Leu Leu Glu Gly Asn Leu Val  
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 Thr Leu Ser Cys Glu Thr Lys Leu Leu Leu Gln Arg Pro Gly Leu Gln  
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 Leu Tyr Phe Ser Phe Tyr Met Gly Ser Lys Thr Leu Arg Gly Arg Asn  
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 Thr Ser Ser Glu Tyr Gln Ile Leu Thr Ala Arg Arg Glu Asp Ser Gly  
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 Leu Tyr Trp Cys Glu Ala Ala Thr Glu Asp Gly Asn Val Leu Lys Arg  
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 Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro  
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 Val Trp Phe His Val Leu Phe Tyr Leu Ala Val Gly Ile Met Phe Leu  
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 Val Asn Thr Val Leu Trp Val Thr Ile Arg Lys Glu Leu Lys Arg Lys  
   305                                      310                                      315                                      320  
 Lys Lys Trp Asp Leu Glu Ile Ser Leu Asp Ser Gly His Glu Lys Lys  
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 Val Thr Ser Ser Leu Gln Glu Asp Arg His Leu Glu Glu Glu Leu Lys  
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25 30 35  
tat cca tca atg ggc atc tta aca cag gtg gag tgg ttc aag atc ggg 317  
Tyr Pro Ser Met Gly Ile Leu Thr Gln Val Glu Trp Phe Lys Ile Gly  
40 45 50  
acc cag cag gat tcc ata gcc att ttc agc cct act cat ggc atg gtc 365  
Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser Pro Thr His Gly Met Val  
55 60 65 70  
ata agg aag ccc tat gct gag agg gtt tac ttt ttg aat tca acg atg 413  
Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr Phe Leu Asn Ser Thr Met  
75 80 85  
gct tcc aat aac atg act ctt ttc ttt cgg aat gcc tct gaa gat gat 461  
Ala Ser Asn Asn Met Thr Leu Phe Phe Arg Asn Ala Ser Glu Asp Asp  
90 95 100  
gtt ggc tac tat tcc tgc tct ctt tac act tac cca cag gga act tgg 509  
Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr Tyr Pro Gln Gly Thr Trp  
105 110 115  
cag aag gtg ata cag gtg gtt cag tca gat agt ttt gag gca gct gtg 557  
Gln Lys Val Ile Gln Val Val Gln Ser Asp Ser Phe Glu Ala Ala Val  
120 125 130  
cca tca aat agc cac att gtt tcg gaa cct gga aag aat gtc aca ctc 605  
Pro Ser Asn Ser His Ile Val Ser Glu Pro Gly Lys Asn Val Thr Leu  
135 140 145 150  
act tgt cag cct cag atg acg tgg cct gtg cag gca gtg agg tgg gaa 653  
Thr Cys Gln Pro Gln Met Thr Trp Pro Val Gln Ala Val Arg Trp Glu  
155 160 165

11-88L.ST25.txt

aag atc cag ccc cgt cag atc gac ctc tta act tac tgc aac ttg gtc Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu Thr Tyr Cys Asn Leu Val	701
cat ggc aga aat ttc acc tcc aag ttc cca aga caa ata gtg agc aac His Gly Arg Asn Phe Thr Ser Lys Phe Pro Arg Gln Ile Val Ser Asn	749
tgc agc cac gga agg tgg agc gtc atc gtc atc ccc gat gtc aca gtc Cys Ser His Gly Arg Trp Ser Val Ile Val Ile Pro Asp Val Thr Val	797
tca gac tcg ggg ctt tac cgc tgc tac ttg cag gcc agc gca gga gaa Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu Gln Ala Ser Ala Gly Glu	845
aac gaa acc ttc gtg atg aga ttg act gta gcc gag ggt aaa acc gat Asn Glu Thr Phe Val Met Arg Leu Thr Val Ala Glu Gly Lys Thr Asp	893
aac caa tat acc ctc ttt gtg gct gga ggg aca gtt tta ttg ttg ttg Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly Thr Val Leu Leu Leu Leu	941
ttt gtt atc tca att acc acc atc att gtc att ttc ctt aac aga agg Phe Val Ile Ser Ile Thr Thr Ile Ile Val Ile Phe Leu Asn Arg Arg	989
aga agg aga gag aga aga gat cta ttt aca gag tcc tgg gat aca cag Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr Glu Ser Trp Asp Thr Gln	1037
aag gca ccc aat aac tat aga agt ccc atc tct acc ggt caa cct acc Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile Ser Thr Gly Gln Pro Thr	1085
aat caa tcc atg gat gat aca aga gag gat att tat gtc aac tat cca Asn Gln Ser Met Asp Asp Thr Arg Glu Asp Ile Tyr Val Asn Tyr Pro	1133
acc ttc tct cgc aga cca aag act aga gtt taagcttatt cttgacatga Thr Phe Ser Arg Arg Pro Lys Thr Arg Val	1183
gtgcattagt aatgactctt atgtactcat gcatggatct ttatgcaatt tttttccact	1243
acccaaggctc taccttagat actagttgtc tgaattgagt tactttgata ggaaaaatac	1303
ttcattacct aaaatcattt ttcatagaac tgtttcagaa aacctgactc taactggttt	1363
atatacaaaa gaaaacttac tgtatcatat aacagaatga tccaggggag attaaagcttt	1423
gggcaagggc tatttaccag ggcttaaatg ttgtgtctag aattaagtat gggcataaac	1483
tggtcttctga atccctttcc agagtgttgg atccatttcc ctggtcttgg cctcactctc	1543
atgcaggctt tcctcttgtg ttggcaagat ggctgccaac tcttggcaat tcatacatcc	1603
ttgtttctgt ctggtagaga gtttgcttct caaatggagc aaacaaattt gattatTTTT	1663
tcattgttaa ataggcaaca tgaccataaa ggatggaatg gcttaagtaa a	1714

<210> 25  
 <211> 336  
 <212> PRT  
 <213> Homo sapiens

<400> 25

Met Asp Tyr Pro Thr Leu Leu Leu Ala Leu Leu His Val Tyr Arg Ala  
 1 5 10 15

Leu Cys Glu Glu Val Leu Trp His Thr Ser Val Pro Phe Ala Glu Asn  
 20 25 30

Met Ser Leu Glu Cys Val Tyr Pro Ser Met Gly Ile Leu Thr Gln Val  
 35 40 45

Glu Trp Phe Lys Ile Gly Thr Gln Gln Asp Ser Ile Ala Ile Phe Ser  
 50 55 60

Pro Thr His Gly Met Val Ile Arg Lys Pro Tyr Ala Glu Arg Val Tyr  
 65 70 75 80

Phe Leu Asn Ser Thr Met Ala Ser Asn Asn Met Thr Leu Phe Phe Arg  
 85 90 95

Asn Ala Ser Glu Asp Asp Val Gly Tyr Tyr Ser Cys Ser Leu Tyr Thr  
 100 105 110

Tyr Pro Gln Gly Thr Trp Gln Lys Val Ile Gln Val Val Gln Ser Asp  
 115 120 125

Ser Phe Glu Ala Ala Val Pro Ser Asn Ser His Ile Val Ser Glu Pro  
 130 135 140

Gly Lys Asn Val Thr Leu Thr Cys Gln Pro Gln Met Thr Trp Pro Val  
 145 150 155 160

Gln Ala Val Arg Trp Glu Lys Ile Gln Pro Arg Gln Ile Asp Leu Leu  
 165 170 175

Thr Tyr Cys Asn Leu Val His Gly Arg Asn Phe Thr Ser Lys Phe Pro  
 180 185 190

Arg Gln Ile Val Ser Asn Cys Ser His Gly Arg Trp Ser Val Ile Val  
 195 200 205

Ile Pro Asp Val Thr Val Ser Asp Ser Gly Leu Tyr Arg Cys Tyr Leu  
 210 215 220

11-88L.ST25.txt

Gln Ala Ser Ala Gly Glu Asn Glu Thr Phe Val Met Arg Leu Thr Val  
225 230 235 240

Ala Glu Gly Lys Thr Asp Asn Gln Tyr Thr Leu Phe Val Ala Gly Gly  
245 250 255

Thr Val Leu Leu Leu Leu Phe Val Ile Ser Ile Thr Thr Ile Ile Val  
260 265 270

Ile Phe Leu Asn Arg Arg Arg Arg Glu Arg Arg Asp Leu Phe Thr  
275 280 285

Glu Ser Trp Asp Thr Gln Lys Ala Pro Asn Asn Tyr Arg Ser Pro Ile  
290 295 300

Ser Thr Gly Gln Pro Thr Asn Gln Ser Met Asp Asp Thr Arg Glu Asp  
305 310 315 320

Ile Tyr Val Asn Tyr Pro Thr Phe Ser Arg Arg Pro Lys Thr Arg Val  
325 330 335

<210> 26  
<211> 2107  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (35)..(1975)

<400> 26  
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1 5  
ctc ctg ctc ctg gtt cta gaa tac ttg gct ttc tct gac tca agt aaa 103  
Leu Leu Leu Leu Val Leu Glu Tyr Leu Ala Phe Ser Asp Ser Ser Lys  
10 15 20  
tgg gtt ttt gag cac cct gaa acc ctc tac gcc tgg gag ggg gcc tgc 151  
Trp Val Phe Glu His Pro Glu Thr Leu Tyr Ala Trp Glu Gly Ala Cys  
25 30 35  
gtc tgg atc ccc tgc acc tac aga gcc cta gat ggt gac ctg gaa agc 199  
Val Trp Ile Pro Cys Thr Tyr Arg Ala Leu Asp Gly Asp Leu Glu Ser  
40 45 50 55  
ttc atc ctg ttc cac aat cct gag tat aac aag aac acc tcg aag ttt 247  
Phe Ile Leu Phe His Asn Pro Glu Tyr Asn Lys Asn Thr Ser Lys Phe  
60 65 70  
gat ggg aca aga ctc tat gaa agc aca aag gat ggg aag gtt cct tct 295  
Asp Gly Thr Arg Leu Tyr Glu Ser Thr Lys Asp Gly Lys Val Pro Ser  
75 80 85



## 11-88L.ST25.txt

gag Glu	cag Gln	aaa Lys 90	agg Arg	gtg Val	caa Gln	ttc Phe	ctg Leu 95	gga Gly	gac Asp	aag Lys	aat Asn 100	aag Lys 100	aac Asn	tgc Cys	aca Thr	343
ctg Leu	agt Ser 105	atc Ile	cac His	ccg Pro	gtg Val	cac His 110	ctc Leu	aat Asn	gac Asp	agt Ser	ggt Gly 115	cag Gln	ctg Leu	ggg Gly	ctg Leu	391
agg Arg 120	atg Met	gag Glu	tcc Ser	aag Lys	act Thr 125	gag Glu	aaa Lys	tgg Trp	atg Met	gaa Glu 130	cga Arg	ata Ile	cac His	ctc Leu	aat Asn 135	439
gtc Val	tct Ser	gaa Glu	agg Arg	cct Pro 140	ttt Phe	cca Pro	cct Pro	cat His	atc Ile 145	cag Gln	ctc Leu	cct Pro	cca Pro	gaa Glu 150	att Ile	487
caa Gln	gag Glu	tcc Ser	cag Gln 155	gaa Glu	gtc Val	act Thr	ctg Leu	acc Thr 160	tgc Cys	ttg Leu	ctg Leu	aat Asn	ttc Phe 165	tcc Ser	tgc Cys	535
tat Tyr	ggg Gly	tat Tyr 170	ccg Pro	atc Ile	caa Gln	ttg Leu	cag Gln 175	tgg Trp	ctc Leu	cta Leu	gag Glu	ggg Gly 180	gtt Val	cca Pro	atg Met	583
agg Arg 185	cag Gln	gct Ala	gct Ala	gtc Val	acc Thr	tcg Ser 190	acc Thr	tcc Ser	ttg Leu	acc Thr	atc Ile 195	aag Lys	tct Ser	gtc Val	ttc Phe	631
acc Thr 200	cgg Arg	agc Ser	gag Glu	ctc Leu	aag Lys 205	ttc Phe	tcc Ser	cca Pro	cag Gln	tgg Trp 210	agt Ser	cac His	cat His	ggg Gly	aag Lys 215	679
att Ile	gtg Val	acc Thr	tgc Cys	cag Gln 220	ctt Leu	cag Gln	gat Asp	gca Ala	gat Asp 225	ggg Gly	aag Lys	ttc Phe	ctc Leu	tcc Ser 230	aat Asn	727
gac Asp	acg Thr	gtg Val	cag Gln 235	ctg Leu	aac Asn	gtg Val	aag Lys	cat His 240	cct Pro	ccc Pro	aag Lys	aag Lys	gtg Val 245	acc Thr	aca Thr	775
gtg Val	att Ile	caa Gln 250	aac Asn	ccc Pro	atg Met	ccg Pro	att Ile 255	cga Arg	gaa Glu	gga Gly	gac Asp	aca Thr 260	gtg Val	acc Thr	ctt Leu	823
tcc Ser	tgt Cys 265	aac Asn	tac Tyr	aat Asn	tcc Ser	agt Ser 270	aac Asn	ccc Pro	agt Ser	gtt Val	acc Thr 275	cgg Arg	tat Tyr	gaa Glu	tgg Trp	871
aaa Lys 280	ccc Pro	cat His	ggc Gly	gcc Ala	tgg Trp 285	gag Glu	gag Glu	cca Pro	tcg Ser	ctt Leu 290	ggg Gly	gtg Val	ctg Leu	aag Lys	atc Ile 295	919
caa Gln	aac Asn	gtt Val	ggc Gly	tgg Trp 300	gac Asp	aac Asn	aca Thr	acc Thr	atc Ile 305	gcc Ala	tgc Cys	gca Ala	gct Ala	tgt Cys 310	aat Asn	967
agt Ser	tgg Trp	tgc Cys	tcg Ser 315	tgg Trp	gcc Ala	tcc Ser	cct Pro	gtc Val 320	gcc Ala	ctg Leu	aat Asn	gtc Val	cag Gln 325	tat Tyr	gcc Ala	1015
ccc Pro	cga Arg	gac Asp 330	gtg Val	agg Arg	gtc Val	cgg Arg	aaa Lys 335	atc Ile	aag Lys	ccc Pro	ctt Leu	tcc Ser 340	gag Glu	att Ile	cac His	1063

11-88L.ST25.txt

tct Ser	gga Gly 345	aac Asn	tcg Ser	gtc Val	agc Ser	ctc Leu 350	caa Gln	tgt Cys	gac Asp	ttc Phe	tca Ser 355	agc Ser	agc Ser	cac His	ccc Pro	1111
aaa Lys 360	gaa Glu	gtc Val	cag Gln	ttc Phe	ttc Phe 365	tgg Trp	gag Glu	aaa Lys	aat Asn	ggc Gly 370	agg Arg	ctt Leu	ctg Leu	ggg Gly 375	aaa Lys 375	1159
gaa Glu	agc Ser	cag Gln	ctg Leu	aat Asn 380	ttt Phe	gac Asp	tcc Ser	atc Ile	tcc Ser 385	cca Pro	gaa Glu	gat Asp	gct Ala	ggg Gly 390	agt Ser	1207
tac Tyr	agc Ser	tgc Cys	tgg Trp 395	gtg Val	aac Asn	aac Asn	tcc Ser	ata Ile 400	gga Gly	cag Gln	aca Thr	gcg Ala	tcc Ser 405	aag Lys	gcc Ala	1255
tgg Trp	aca Thr	ctt Leu 410	gaa Glu	gtg Val	ctg Leu	tat Tyr	gca Ala 415	ccc Pro	agg Arg	agg Arg	ctg Leu	cgt Arg 420	gtg Val	tcc Ser	atg Met	1303
agc Ser	ccg Pro 425	ggg Gly	gac Asp	caa Gln	gtg Val	atg Met 430	gag Glu	ggg Gly	aag Lys	agt Ser	gca Ala 435	acc Thr	ctg Leu	acc Thr	tgt Cys	1351
gag Glu 440	agc Ser	gac Asp	gcc Ala	aac Asn	cct Pro 445	ccc Pro	gtc Val	tcc Ser	cac His	tac Tyr 450	acc Thr	tgg Trp	ttt Phe	gac Asp	tgg Trp 455	1399
aat Asn	aac Asn	caa Gln	agc Ser	ctc Leu 460	ccc Pro	tac Tyr	cac His	agc Ser	cag Gln 465	aag Lys	ctg Leu	aga Arg	ttg Leu	gag Glu 470	ccg Pro	1447
gtg Val	aag Lys	gtc Val	cag Gln 475	cac His	tcg Ser	ggt Gly	gcc Ala	tac Tyr 480	tgg Trp	tgc Cys	cag Gln	ggg Gly	acc Thr 485	aac Asn	agt Ser	1495
gtg Val	ggc Gly	aag Lys 490	ggc Gly	cgt Arg	tcg Ser	cct Pro	ctc Leu 495	agc Ser	acc Thr	ctc Leu	acc Thr	gtc Val 500	tac Tyr	tat Tyr	agc Ser	1543
ccg Pro	gag Glu 505	acc Thr	atc Ile	ggc Gly	agg Arg	cga Arg 510	gtg Val	gct Ala	gtg Val	gga Gly	ctc Leu 515	ggg Gly	tcc Ser	tgc Cys	ctc Leu	1591
gcc Ala 520	atc Ile	ctc Leu	atc Ile	ctg Leu	gca Ala 525	atc Ile	tgt Cys	ggg Gly	ctc Leu	aag Lys 530	ctc Leu	cag Gln	cga Arg	cgt Arg	tgg Trp 535	1639
aag Lys	agg Arg	aca Thr	cag Gln	agc Ser 540	cag Gln	cag Gln	ggg Gly	ctt Leu	cag Gln 545	gag Glu	aat Asn	tcc Ser	agc Ser	ggc Gly 550	cag Gln	1687
agc Ser	ttc Phe	ttt Phe	gtg Val 555	agg Arg	aat Asn	aaa Lys	aag Lys	gtt Val 560	aga Arg	agg Arg	gcc Ala	ccc Pro	ctc Leu 565	tct Ser	gaa Glu	1735
ggc Gly	ccc Pro	cac His 570	tcc Ser	ctg Leu	gga Gly	tgc Cys	tac Tyr 575	aat Asn	cca Pro	atg Met	atg Met	gaa Glu 580	gat Asp	ggc Gly	att Ile	1783
agc Ser	tac Tyr	acc Thr	acc Thr	ctg Leu	cgc Arg	ttt Phe	ccc Pro	gag Glu	atg Met	aac Asn	ata Ile	cca Pro	cga Arg	act Thr	gga Gly	1831

11-88L.ST25.txt  
595

585

590

gat	gca	gag	tcc	tca	gag	atg	cag	aga	cct	ccc	ccg	gac	tgc	gat	gac	1879
Asp	Ala	Glu	Ser	Ser	Glu	Met	Gln	Arg	Pro	Pro	Pro	Asp	Cys	Asp	Asp	
600					605					610					615	
acg	gtc	act	tat	tca	gca	ttg	cac	aag	cgc	caa	gtg	ggc	act	atg	aga	1927
Thr	Val	Thr	Tyr	Ser	Ala	Leu	His	Lys	Arg	Gln	Val	Gly	Thr	Met	Arg	
				620					625					630		
acg	tca	ttc	cag	att	ttc	cag	aag	atg	agg	gga	ttc	att	act	cag	agc	1975
Thr	Ser	Phe	Gln	Ile	Phe	Gln	Lys	Met	Arg	Gly	Phe	Ile	Thr	Gln	Ser	
			635					640					645			
tgatccagtt	tggggtcggg	gagcggcctc	aggcacaaga	aaatgtggac	tatgtgatcc											2035
tcaaacattg	acactggatg	ggctgcagca	gaggcactgg	gggcagcggg	ggccagggaa											2095
gtccccgagt	tt															2107

<210> 27  
<211> 647  
<212> PRT  
<213> Homo sapiens

<400> 27

Met	His	Leu	Leu	Gly	Pro	Trp	Leu	Leu	Leu	Leu	Val	Leu	Glu	Tyr	Leu	
1				5					10					15		
Ala	Phe	Ser	Asp	Ser	Ser	Lys	Trp	Val	Phe	Glu	His	Pro	Glu	Thr	Leu	
			20					25					30			
Tyr	Ala	Trp	Glu	Gly	Ala	Cys	Val	Trp	Ile	Pro	Cys	Thr	Tyr	Arg	Ala	
		35					40					45				
Leu	Asp	Gly	Asp	Leu	Glu	Ser	Phe	Ile	Leu	Phe	His	Asn	Pro	Glu	Tyr	
	50					55					60					
Asn	Lys	Asn	Thr	Ser	Lys	Phe	Asp	Gly	Thr	Arg	Leu	Tyr	Glu	Ser	Thr	
65					70				75						80	
Lys	Asp	Gly	Lys	Val	Pro	Ser	Glu	Gln	Lys	Arg	Val	Gln	Phe	Leu	Gly	
				85					90					95		
Asp	Lys	Asn	Lys	Asn	Cys	Thr	Leu	Ser	Ile	His	Pro	Val	His	Leu	Asn	
			100					105					110			
Asp	Ser	Gly	Gln	Leu	Gly	Leu	Arg	Met	Glu	Ser	Lys	Thr	Glu	Lys	Trp	
		115					120					125				
Met	Glu	Arg	Ile	His	Leu	Asn	Val	Ser	Glu	Arg	Pro	Phe	Pro	Pro	His	
	130					135					140					

11-88L.ST25.txt

Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr  
145 150 155 160

Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp  
165 170 175

Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser  
180 185 190

Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro  
195 200 205

Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala  
210 215 220

Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His  
225 230 235 240

Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile Arg  
245 250 255

Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn Pro  
260 265 270

Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu Pro  
275 280 285

Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr Thr  
290 295 300

Ile Ala Cys Ala Ala Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro Val  
305 310 315 320

Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys Ile  
325 330 335

Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln Cys  
340 345 350

Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu Lys  
355 360 365

Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser Ile  
370 375 380

Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser Ile  
385 390 395 400

11-88L.ST25.txt

Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala Pro  
405 410 415

Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu Gly  
420 425 430

Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val Ser  
435 440 445

His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro Tyr His Ser  
450 455 460

Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala Tyr  
465 470 475 480

Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu Ser  
485 490 495

Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val Ala  
500 505 510

Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys Gly  
515 520 525

Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly Leu  
530 535 540

Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Val  
545 550 555 560

Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr Asn  
565 570 575

Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro Glu  
580 585 590

Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln Arg  
595 600 605

Pro Pro Pro Asp Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His Lys  
610 615 620

Arg Gln Val Gly Thr Met Arg Thr Ser Phe Gln Ile Phe Gln Lys Met  
625 630 635 640

Arg Gly Phe Ile Thr Gln Ser

<210> 28  
 <211> 1200  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (101)..(880)

<400> 28  
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 cagcaactgg gcacagaaag gagccgcctg ggcagggacc atg gca cgg cca cat 115  
 Met Ala Arg Pro His  
 1 5  
 ccc tgg tgg ctg tgc gtt ctg ggg acc ctg gtg ggg ctc tca gct act 163  
 Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val Gly Leu Ser Ala Thr  
 10 15 20  
 cca gcc ccc aag agc tgc cca gag agg cac tac tgg gct cag gga aag 211  
 Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr Trp Ala Gln Gly Lys  
 25 30 35  
 ctg tgc tgc cag atg tgt gag cca gga aca ttc ctc gtg aag gac tgt 259  
 Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe Leu Val Lys Asp Cys  
 40 45 50  
 gac cag cat aga aag gct gct cag tgt gat cct tgc ata ccg ggg gtc 307  
 Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro Cys Ile Pro Gly Val  
 55 60 65  
 tcc ttc tct cct gac cac cac acc cgg ccc cac tgt gag agc tgt cgg 355  
 Ser Phe Ser Pro Asp His His Thr Arg Pro His Cys Glu Ser Cys Arg  
 70 75 80 85  
 cac tgt aac tct ggt ctt ctc gtt cgc aac tgc acc atc act gcc aat 403  
 His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys Thr Ile Thr Ala Asn  
 90 95 100  
 gct gag tgt gcc tgt cgc aat ggc tgg cag tgc agg gac aag gag tgc 451  
 Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys Arg Asp Lys Glu Cys  
 105 110 115  
 acc gag tgt gat cct ctt cca aac cct tcg ctg acc gct cgg tcg tct 499  
 Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu Thr Ala Arg Ser Ser  
 120 125 130  
 cag gcc ctg agc cca cac cct cag ccc acc cac tta cct tat gtc agt 547  
 Gln Ala Leu Ser Pro His Pro Gln Pro Thr His Leu Pro Tyr Val Ser  
 135 140 145  
 gag atg ctg gag gcc agg aca gct ggg cac atg cag act ctg gct gac 595  
 Glu Met Leu Glu Ala Arg Thr Ala Gly His Met Gln Thr Leu Ala Asp  
 150 155 160 165  
 ttc agg cag ctg cct gcc cgg act ctc tct acc cac tgg cca ccc caa 643  
 Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr His Trp Pro Pro Gln  
 170 175 180

11-88L.ST25.txt

aga tcc ctg tgc agc tcc gat ttt att cgc atc ctt gtg atc ttc tct	691
Arg Ser Leu Cys 185 Ser Ser Asp Phe 190 Arg Ile Leu Val 195 Ile Phe Ser	
gga atg ttc ctt gtt ttc acc ctg gcc ggg gcc ctg ttc ctc cat caa	739
Gly Met Phe 200 Leu Val Phe Thr Leu 205 Ala Gly Ala Leu Phe 210 Leu His Gln	
cga agg aaa tat aga tca aac aaa gga gaa agt cct gtg gag cct gca	787
Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu Pro Ala	
215 220 225	
gag cct tgt cgt tac agc tgc ccc agg gag gag gag ggc agc acc atc	835
Glu Pro Cys Arg Tyr 235 Ser Cys Pro Arg Glu Glu Glu Gly Ser Thr Ile	
230 240 245	
ccc atc cag gag gat tac cga aaa ccg gag cct gcc tgc tcc ccc	880
Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser Pro	
250 255 260	
tgagccagca cctgcggtag ctgcactaca gccctggcct ccacccccac cccgccgacc	940
atccaagga gagtgagacc tggcagccac aactgcagtc ccattctctt gtcagggccc	1000
tttctgtgt acacgtgaca gagtgccttt tcgagactgg cagggacgag gacaaatatg	1060
gatgaggtgg agagtgggaa gcaggagccc agccagctgc gcgcgcgtgc aggagggcgg	1120
gggctctggt tgtaaggcac acttctgct gcgaaagacc cacatgctac aagacgggca	1180
aaataaagtg acagatgacc	1200

<210> 29  
 <211> 260  
 <212> PRT  
 <213> Homo sapiens

<400> 29

Met Ala Arg Pro His Pro Trp Trp Leu Cys Val Leu Gly Thr Leu Val
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Gly Leu Ser Ala Thr Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr
20 25 30
Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe
35 40 45
Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro
50 55 60
Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
65 70 75 80
Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
85 90 95

11-88L.ST25.txt

Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys  
100 105 110

Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu  
115 120 125

Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His  
130 135 140

Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met  
145 150 155 160

Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr  
165 170 175

His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile  
180 185 190

Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala  
195 200 205

Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser  
210 215 220

Pro Val Glu Pro Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu  
225 230 235 240

Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro  
245 250 255

Ala Cys Ser Pro  
260

<210> 30  
<211> 2350  
<212> DNA  
<213> Homo sapiens

<400> 30  
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aagaactaga gaaggaccaa gcaaagccat gatattttcca tggaaatgtc agagcaccca 120  
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## 11-88L.ST25.txt

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## 11-88L.ST25.txt

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 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu  
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 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val  
 20 25 30

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gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310  
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 70 75 80

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 Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys  
 85 90 95

gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag 454  
 Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln  
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tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt 502  
 Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys  
 115 120 125

aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata 550  
 Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile  
 130 135 140 145

act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac 598  
 Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr  
 150 155 160

11-88L.ST25.txt

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atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt Ile Phe 195 Tyr Thr Phe Ser Thr 200 Val His Pro Ile Pro 205 Asp Glu Asp Ser	742
ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa Pro Trp Ile Thr Asp Ser 215 Thr Asp Arg Ile Pro 220 Ala Thr Arg Asp Gln 225	790
gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gaa tct gaa Asp Thr Phe His Pro 230 Ser Gly Gly Ser His 235 Thr Thr His Glu Ser 240 Glu	838
tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc Ser Asp Gly His 245 Ser His Gly Ser Gln 250 Glu Gly Gly Ala Asn Thr Thr	886
tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ttg Ser Gly Pro 260 Ile Arg Thr Pro 265 Gln Ile Pro Glu Trp 270 Leu Ile Ile Leu	934
gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt tgc att gca gtc Ala Ser 275 Leu Leu Ala Leu Ala Leu Ile Leu Ala Val 285 Cys Ile Ala Val	982
aac agt cga aga agg tgt ggg cag aag aaa aag cta gtg atc aac agt Asn Ser Arg Arg Arg Cys 295 Gly Gln Lys Lys Lys 300 Leu Val Ile Asn Ser 305	1030
ggc aat gga gct gtg gag gac aga aag cca agt gga ctc aac gga gag Gly Asn Gly Ala 310 Val Glu Asp Arg Lys Pro 315 Ser Gly Leu Asn Gly 320 Glu	1078
gcc agc aag tct cag gaa atg gtg cat ttg gtg aac aag gag tcg tca Ala Ser Lys Ser 325 Gln Glu Met Val His 330 Leu Val Asn Lys Glu Ser Ser	1126
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aat gtg gac atg aag att ggg gtg taacacctac accattatct tggaagaaa Asn Val 355 Asp Met Lys Ile Gly Val 360	1228
caaccgttgt aaacataacc attacagga gctgggacac ttaacagatg caatgtgcta	1288
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&lt;400&gt; 32

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20      25      30
Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
35      40      45
Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
50      55      60
Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
65      70      75      80
Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
85      90      95
Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
100     105     110
Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
115     120     125
Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
130     135     140
Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
145     150     155     160
Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
165     170     175
Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
180     185     190
Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
195     200     205
Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp
210     215     220
Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Glu Ser
225     230     235     240

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11-88L.ST25.txt

Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr  
245 250 255

Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile  
260 265 270

Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala  
275 280 285

Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn  
290 295 300

Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly  
305 310 315 320

Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser  
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Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu  
5 10 15

agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214  
Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val  
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ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262  
Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala  
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gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310

## 11-88L.ST25.txt

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gca Ala	gca Ala	aac Asn 100	aac Asn	aca Thr	ggg Gly	gtg Val	tac Tyr 105	atc Ile	ctc Leu	aca Thr	tac Tyr	aac Asn 110	acc Thr	tcc Ser	cag Gln	454
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aca Thr 130	tca Ser	gtc Val	aca Thr	gac Asp	ctg Leu 135	ccc Pro	aat Asn	gcc Ala	ttt Phe	gat Asp 140	gga Gly	cca Pro	att Ile	acc Thr	ata Ile 145	550
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aga Arg	acg Thr	aat Asn	cct Pro 165	gaa Glu	gac Asp	atc Ile	tac Tyr	ccc Pro 170	agc Ser	aac Asn	cct Pro	act Thr	gat Asp 175	gat Asp	gac Asp	646
gtg Val	agc Ser	agc Ser 180	ggc Gly	tcc Ser	tcc Ser	agt Ser	gaa Glu 185	agg Arg	agc Ser	agc Ser	act Thr	tca Ser 190	gga Gly	ggt Gly	tac Tyr	694
atc Ile	ttt Phe 195	tac Tyr	acc Thr	ttt Phe	tct Ser	act Thr 200	gta Val	cac His	ccc Pro	atc Ile	cca Pro 205	gac Asp	gaa Glu	gac Asp	agt Ser	742
ccc Pro 210	tgg Trp	atc Ile	acc Thr	gac Asp	agc Ser 215	aca Thr	gac Asp	aga Arg	atc Ile	cct Pro 220	cgt Arg	acc Thr	aat Asn	atg Met	gac Asp 225	790
tcc Ser	agt Ser	cat His	agt Ser	aca Thr 230	acg Thr	ctt Leu	cag Gln	cct Pro	act Thr 235	gca Ala	aat Asn	cca Pro	aac Asn	aca Thr 240	ggt Gly	838
ttg Leu	gtg Val	gaa Glu	gat Asp 245	ttg Leu	gac Asp	agg Arg	aca Thr	gga Gly 250	cct Pro	ctt Leu	tca Ser	atg Met	aca Thr 255	acg Thr	cag Gln	886
cag Gln	agt Ser	aat Asn 260	tct Ser	cag Gln	agc Ser	ttc Phe	tct Ser 265	aca Thr	tca Ser	cat His	gaa Glu	ggc Gly 270	ttg Leu	gaa Glu	gaa Glu	934
gat Asp	aaa Lys 275	gac Asp	cat His	cca Pro	aca Thr	act Thr 280	tct Ser	act Thr	ctg Leu	aca Thr	tca Ser 285	agc Ser	aat Asn	agg Arg	aat Asn	982
gat Asp 290	gtc Val	aca Thr	ggt Gly	gga Gly	aga Arg 295	aga Arg	gac Asp	cca Pro	aat Asn	cat His 300	tct Ser	gaa Glu	ggc Gly	tca Ser	act Thr 305	1030

## 11-88L.ST25.txt

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agg acc ttc atc cca gtg acc tca gct aag act ggg tcc ttt gga gtt	1126
Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr Gly Ser Phe Gly Val	
325 330 335	
act gca gtt act gtt gga gat tcc aac tct aat gtc aat cgt tcc tta	1174
Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser Leu	
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tca gga gac caa gac aca ttc cac ccc agt ggg ggg tcc cat acc act	1222
Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr	
355 360 365	
cat gga tct gaa tca gat gga cac tca cat ggg agt caa gaa ggt gga	1270
His Gly Ser Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly	
370 375 380 385	
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Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp	
390 395 400	
ctg atc atc ttg gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt	1366
Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val	
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Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu	
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Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser Gly	
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ctc aac gga gag gcc agc aag tct cag gaa atg gtg cat ttg gtg aac	1510
Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val Asn	
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aag gag tcg tca gaa act cca gac cag ttt atg aca gct gat gag aca	1558
Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met Thr Ala Asp Glu Thr	
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Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly Val	
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11-88L.ST25.txt

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Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu  
 35 40 45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala  
 50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly  
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Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile  
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Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser  
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Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp  
 115 120 125

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr  
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Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp  
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Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly  
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11-88L.ST25.txt

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 Asp Ser Ser His Ser Thr Thr Leu Gln Pro Thr Ala Asn Pro Asn Thr  
 225 230 235 240  
 Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu Ser Met Thr Thr  
 245 250  
 Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His Glu Gly Leu Glu  
 260 265 270  
 Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr Ser Ser Asn Arg  
 275 280 285  
 Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His Ser Glu Gly Ser  
 290 295 300  
 Thr His Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro His Thr Lys Glu  
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 325 330 335  
 Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn Val Asn Arg Ser  
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 355 360 365  
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 370 375 380  
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 Trp Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala  
 405 410 415  
 Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly Gln Lys Lys Lys  
 420 425 430  
 Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp Arg Lys Pro Ser

435

440

Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met Val His Leu Val  
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15 20 25

ggc ttt ggg atc tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc 205  
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His Asn Leu Pro Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly  
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tct att atc atg gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag 301  
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65 70 75

gaa aac aag tgt ctg ctt atg tcg ttc ttc atc ctg ctg ctg att atc 349  
Glu Asn Lys Cys Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile  
80 85 90

ctc ctt gct gag gtg acc ttg gcc atc ctg ctc ttt gta tat gaa cag 397  
Leu Leu Ala Glu Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln  
95 100 105

aag ctg aat gag tat gtg gct aag ggt ctg acc gac agc atc cac cgt 445  
Lys Leu Asn Glu Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg  
110 115 120

tac cac tca gac aat agc acc aag gca gcg tgg gac tcc atc cag tca 493  
Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser  
125 130 135 140

11-88L.ST25.txt

ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg acc agt ggc	541
Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly	
145 150 155	
cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt tgc tat gcg	589
Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala	
160 165 170	
aaa gca aga ctg tgg ttt cat tcc aat ttc ctg tat atc gga atc atc	637
Lys Ala Arg Leu Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile	
175 180 185	
acc atc tgt gta tgt gtg att gag gtg ttg ggg atg tcc ttt gca ctg	685
Thr Ile Cys Val Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu	
190 195 200	
acc ctg aac tgc cag att gac aaa acc agc cag acc ata ggg cta	730
Thr Leu Asn Cys Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu	
205 210 215	
tgatctgcag tagttctgtg gtgaagagac ttgtttcatc tccggaaatg caaaaccatt	790
tatagcatga agccctacat gatcactgca ggatgatcct cctcccatcc tttccctttt	850
taggtccctg tcttatacaa ccagagaagt ggggtgttggc caggcacatc ccatctcagg	910
cagcaagaca atcttttact cactgacggc agcagccatg tctctcaaag tggtgaaact	970
aatatctgag catcttttag acaagagagg caaagacaaa ctggatttaa tggcccaaca	1030
tcaaaggggtg aaccaggat atgaattttt gcactctccc attgtcgaat tagtctccag	1090
cctctaaata atgcccagtc ttctcccaa agtcaagcaa gagactagtt gaagggagtt	1150
ctggggccag gctcactgga ccattgtcac aaccctctgt ttctctttga ctaagtgcc	1210
tggctacagg aattacacag ttctctttct ccaaagggca agatctcatt tcaatttctt	1270
tattagaggg ccttattgat gtgttctaag tctttccaga aaaaaactat ccagtgattt	1330
atatcctgat ttcaaccagt cacttagctg ataatcacag taagaagact tctggtatta	1390
tctctctatc agataagatt ttgttaatgt actattttac tcttcaataa ataaaacagt	1450
tt	1452

<210> 36  
 <211> 219  
 <212> PRT  
 <213> Homo sapiens

<400> 36

Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe  
 1 5 10 15

Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile  
 20 25 30

Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro  
 35 40 45

Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met  
 50 55 60

Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys  
 65 70 75 80

Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu  
 85 90 95

Val Thr Leu Ala Ile Leu Leu Phe Val Tyr Glu Gln Lys Leu Asn Glu  
 100 105 110

Tyr Val Ala Lys Gly Leu Thr Asp Ser Ile His Arg Tyr His Ser Asp  
 115 120 125

Asn Ser Thr Lys Ala Ala Trp Asp Ser Ile Gln Ser Phe Leu Gln Cys  
 130 135 140

Cys Gly Ile Asn Gly Thr Ser Asp Trp Thr Ser Gly Pro Pro Ala Ser  
 145 150 155 160

Cys Pro Ser Asp Arg Lys Val Glu Gly Cys Tyr Ala Lys Ala Arg Leu  
 165 170 175

Trp Phe His Ser Asn Phe Leu Tyr Ile Gly Ile Ile Thr Ile Cys Val  
 180 185 190

Cys Val Ile Glu Val Leu Gly Met Ser Phe Ala Leu Thr Leu Asn Cys  
 195 200 205

Gln Ile Asp Lys Thr Ser Gln Thr Ile Gly Leu  
 210 215

<210> 37

<211> 12

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide primer

<400> 37

ctttagagca ca

12

<210> 38

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic peptide

<220>

<221> VARIANT

<222> (1)..(9)

<223> Xaa at positions 1 and 4 can be any amino acid

<400> 38

Xaa Pro Pro Xaa Ala Ser Ala Leu Pro  
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<210> 39

<211> 240

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Pro Pro Arg Leu Leu Leu Leu Pro Leu Leu Leu Ala Leu  
1 5 10 15

Ala Arg Gly Leu Pro Gly Ala Leu Ala Ala Gln Glu Val Gln Gln Ser  
20 25 30

Pro His Cys Thr Thr Val Pro Val Gly Ala Ser Val Asn Ile Thr Cys  
35 40 45

Ser Thr Ser Gly Gly Leu Arg Gly Ile Tyr Leu Arg Gln Leu Gly Pro  
50 55 60

Gln Pro Gln Asp Ile Ile Tyr Tyr Glu Asp Gly Val Val Pro Thr Thr  
65 70 75 80

Asp Arg Arg Phe Glu Gly Arg Ile Asp Phe Ser Gly Ser Gln Asp Asn  
85 90 95

Leu Thr Ile Thr Met His Arg Leu Gln Leu Ser Asp Thr Gly Thr Tyr  
100 105 110

Thr Cys Gln Ala Ile Thr Glu Val Asn Val Tyr Gly Ser Gly Thr Leu  
115 120 125

Val Leu Val Thr Glu Glu Gln Ser Gln Gly Trp His Arg Cys Ser Asp  
130 135 140

Ala Pro Pro Arg Ala Ser Ala Leu Pro Ala Pro Pro Thr Gly Ser Ala  
145 150 155 160

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Leu Pro Asp Pro Gln Thr Ala Ser Ala Leu Pro Asp Pro Pro Ala Ala  
165 170 175

Ser Ala Leu Pro Ala Ala Leu Ala Val Ile Ser Phe Leu Leu Gly Leu  
180 185 190

Gly Leu Gly Val Ala Cys Val Leu Ala Arg Thr Gln Ile Lys Lys Leu  
195 200 205

Cys Ser Trp Arg Asp Lys Asn Ser Ala Ala Cys Val Val Tyr Glu Asp  
210 215 220

Met Ser His Ser Arg Cys Asn Thr Leu Ser Ser Pro Asn Gln Tyr Gln  
225 230 235 240

<210> 40  
<211> 311  
<212> PRT  
<213> Homo sapiens

<400> 40

Met Ser Gln Asn Val Cys Pro Arg Asn Leu Trp Leu Leu Gln Pro Leu  
1 5 10 15

Thr Val Leu Leu Leu Leu Ala Ser Ala Asp Ser Gln Ala Ala Ala Pro  
20 25 30

Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val Leu Gln  
35 40 45

Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro Glu Ser  
50 55 60

Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr His Thr  
65 70 75 80

Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly Glu Tyr  
85 90 95

Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His Leu Thr  
100 105 110

Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln  
115 120 125

Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp Lys Pro  
130 135 140

11-88L.ST25.txt

Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys Phe Ser  
145 150 155 160

Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser His Ser  
165 170 175

Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe Ser Ser  
180 185 190

Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser Ser Ser  
195 200 205

Pro Met Gly Ile Ile Val Ala Val Val Ile Ala Thr Ala Val Ala Ala  
210 215 220

Ile Val Ala Ala Val Val Ala Leu Ile Tyr Cys Arg Lys Lys Arg Ile  
225 230 235 240

Ser Ala Asn Ser Thr Asp Pro Val Lys Ala Ala Gln Phe Glu Pro Pro  
245 250 255

Gly Arg Gln Met Ile Ala Ile Arg Lys Arg Gln Leu Glu Glu Thr Asn  
260 265 270

Asn Asp Tyr Glu Thr Ala Asp Gly Gly Tyr Met Thr Leu Asn Pro Arg  
275 280 285

Ala Pro Thr Asp Asp Asp Lys Asn Ile Tyr Leu Thr Leu Pro Pro Asn  
290 295 300

Asp His Val Asn Ser Asn Asn  
305 310

<210> 41  
<211> 385  
<212> PRT  
<213> Homo sapiens

<400> 41

Met Gly Cys Arg Arg Thr Arg Glu Gly Pro Ser Lys Ala Met Ile Phe  
1 5 10 15

Pro Trp Lys Cys Gln Ser Thr Gln Arg Asp Leu Trp Asn Ile Phe Lys  
20 25 30

Leu Trp Gly Trp Thr Met Leu Cys Cys Asp Phe Leu Ala His His Gly  
35 40 45

11-88L.ST25.txt

Thr Asp Cys Trp Thr Tyr His Tyr Ser Glu Lys Pro Met Asn Trp Gln  
 50 55 60  
 Arg Ala Arg Arg Phe Cys Arg Asp Asn Tyr Thr Asp Leu Val Ala Ile  
 65 70 75 80  
 Gln Asn Lys Ala Glu Ile Glu Tyr Leu Glu Lys Thr Leu Pro Phe Ser  
 85 90 95  
 Arg Ser Tyr Tyr Trp Ile Gly Ile Arg Lys Ile Gly Gly Ile Trp Thr  
 100 105 110  
 Trp Val Gly Thr Asn Lys Ser Leu Thr Glu Glu Ala Glu Asn Trp Gly  
 115 120 125  
 Asp Gly Glu Pro Asn Asn Lys Lys Asn Lys Glu Asp Cys Val Glu Ile  
 130 135 140  
 Tyr Ile Lys Arg Asn Lys Asp Ala Gly Lys Trp Asn Asp Asp Ala Cys  
 145 150 155 160  
 His Lys Leu Lys Ala Ala Leu Cys Tyr Thr Ala Ser Cys Gln Pro Trp  
 165 170 175  
 Ser Cys Ser Gly His Gly Glu Cys Val Glu Ile Ile Asn Asn Tyr Thr  
 180 185 190  
 Cys Asn Cys Asp Val Gly Tyr Tyr Gly Pro Gln Cys Gln Phe Val Ile  
 195 200 205  
 Gln Cys Glu Pro Leu Glu Ala Pro Glu Leu Gly Thr Met Asp Cys Thr  
 210 215 220  
 His Ser Leu Gly Asn Phe Ser Phe Ser Ser Gln Cys Ala Phe Ser Cys  
 225 230 235 240  
 Ser Glu Gly Thr Asn Leu Thr Gly Ile Glu Glu Thr Thr Cys Gly Pro  
 245 250 255  
 Phe Gly Asn Trp Ser Ser Pro Glu Pro Thr Cys Gln Val Ile Gln Cys  
 260 265 270  
 Glu Pro Leu Ser Ala Pro Asp Leu Gly Ile Met Asn Cys Ser His Pro  
 275 280 285  
 Leu Ala Ser Phe Ser Phe Thr Ser Ala Cys Thr Phe Ile Cys Ser Glu  
 290 295 300



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Gly Thr Glu Leu Ile Gly Lys Lys Lys Thr Ile Cys Glu Ser Ser Gly  
305 310 315 320

Ile Trp Ser Asn Pro Ser Pro Ile Cys Gln Lys Leu Asp Lys Ser Phe  
325 330 335

Ser Met Ile Lys Glu Gly Asp Tyr Asn Pro Leu Phe Ile Pro Val Ala  
340 345 350

Val Met Val Thr Ala Phe Ser Gly Leu Ala Phe Ile Ile Trp Leu Ala  
355 360 365

Arg Arg Leu Lys Lys Gly Lys Lys Ser Lys Arg Ser Met Asn Asp Pro  
370 375 380

Tyr  
385